

sequence encoding a polypeptide having fumonisin esterase activity and a sequence encoding a polypeptide having amine oxidase activity; and,

b) stably integrating into the genome of said plant cell a secondary nucleotide sequence operably linked to a second promoter active in said plant cell, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

3. The method of claim 1, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyamine oxidase.

8. The method of claim 1, wherein at least one of said first promoter and said second promoter is an inducible promoter.

9. The method of claim 8 further comprising inducing expression of said primary and said secondary nucleotide sequences for a time sufficient to reduce pathogenicity of said fungus.

10. A plant having stably integrating into its genome  
a) a primary nucleotide sequence operably linked to a promoter active in said plant, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,  
b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

12. The plant of claim 10, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyamine oxidase.

13. The plant of claim 10, wherein the primary nucleotide sequence stably incorporated into the plant cell comprises a sequence encoding a polypeptide having fumonisin esterase activity and a sequence encoding a polypeptide having amino oxidase activity.

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17. Transformed seed of the plant of claim 10.

18. A plant cell having stably integrating into its genome

- a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

19. A method of reducing pathogenicity of a fungus that produces fumonisin, comprising stably integrating into the genome of a plant cell:

- a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- b) a secondary nucleotide sequence operably linked to a promoter active in said plant cell, wherein said secondary nucleotide sequence comprises at least one sequence selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4,

7, and 10.

- BI2*  
*cancel*  
*E1*  
*cancel*
20. A plant having stably integrating into its genome
- a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
  - b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence comprises at least one sequence selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4, 7, and 10.
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Please add the following new claims:

- sub*  
*E1*  
*BI3*
21. The method of claim 1, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.
22. The method of claim 1, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.
23. The plant of claim 10, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.
24. The plant of claim 10, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.
25. The plant of claim 10, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

26. The plant cell of claim 18, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

27. The plant cell of claim 18, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

28. The plant cell of claim 18, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

29. The method of claim 8, wherein said first promoter and said second promoter are the same promoter.

30. The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 80% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

31. The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

32. The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 80% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

33. The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

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